



FIG. 1A
FIG. 1B
FIG. 1C

FIG. 1

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1 ATGGAGGCGCGCTTCTTCGCAATCTGTGTCTGGCTGACTCTGCGGAGCTGAAACCCAGGACTCCAGGGCTGTGCCCGGTGGTGC
M G G R V F L A F C V W L T L P G A E T Q D S R G C A R W C
91 CCTCAGAACTCCTCGTGTCAATGCCACCGCTGTGCTGCAATCCAGGGTTCAGCTCTTTCTGAGATCATCACCACCCGACGGAG
P Q S S C V A T A C R C N P G F S S F S E I I T P T E
181 ACTTGTGACGACATCAACGAGTGTGCAACACCGTCCGAAAGTTCATCGCGAAATTCCTCGGACTGCTGGAACACAGAGGGAGCTACGAC
T C D I N E C A T P S K V S C G K F S D C W N T E G S Y D
271 TCGGTGTGACGCGGGATATGAGCCTGTTCTGGGACAAAACATTCAAGATGAGAGCGGAGAACACCTGTCAAGATGTGGACGAATGT
C V C S P G Y E P V S G T K T F K E S E N T C Q D V D E C
361 CAGCAGAACCCAGGCTCTGTAAAGCTACGGCACCTGCGTCAACACCCCTTGGCAGCTATACCTGCCAGTGCCTGCCCTGGCTTCAAGTTC
Q Q N P R L C K S Y G T C V N T L G S Y T C Q C L P G F K F
451 ATACCTGAGGATCCGAAGTCTGCACAGATGTGAATGAATGCACCTCCGGACAAAATCCGTGCCACAGTCCACCCACTGCCTCAACAAAC
I P E D P K V C T D V N E C T S G Q N P C H S S T E C L N N
541 GTGGCAGCTATCAGTGTGCTGCCGACCGGCTGGCAACCGATTCGGGGTCCCCCAATGGCCCAACAATACCGTCTGTGAAGATGTG
V G S Y Q C R C R P C N Q P I P G S P N G P N N T V C E D V
631 GACGAGTGCAGCTCCGGCAGCATCAGTGTGACAGTCCACCGTCTGCTTCAACACCGTGGTTCATACAGTGCCTGCCGCTGCCGCCAGGC
D E C S S G Q H Q C D S S T V C F N T V G S Y S C R C R P G
721 TGAAGCCCGACACGGAATCCCGAATAACCAAGGACACTGTCTGTGAAGATATGACTTCTCCACCTGGACCCCGCCCTGGAGTTC
W K P R H G I P N N Q K D T V C E D M T F S T W T P P G V
811 CACAGCCAGACGCTTCCCGATTCTTCGACAAAGTCCAGGACCTGGGACAGACTCCAGCAAGCTCAGCCGAGGTCCACCATCCAGAAT
H S Q T L S R F F D K V Q D L G R D S K T S S A E V T I Q N

FIG. 1A



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FIG. 1A
FIG. 1B
FIG. 1C

FIG. 1

901 GTCATCAAAATTGGTGATGAACCTGATGGAAGCTCCTGGAGACGTAGAGGCCCTGGCGCCACCTGTCCGGCACCTCATAGCCACCCAGCTG
V I K L V D E L M E A P G D V E A L A P P V R H L I A T Q L 330
991 CTCTCAAACCTTGAAGATATCATGAGGATCCTGGCCAAGAGCCTGCCTAAAGGCCCTTACCTACATTTCCCTTTCGAACACAGAGCTG
L S N L E D I M R I L A K S L P K G P F T Y I S P S N T E L 360
1081 ACCCTGATGATCCAGGAGCGGGGACAAAGAACGTCACTATGGGTGAGAGCAGCGCACGATGAAGCTGAATTGGGCTGTGGCAGCTGGA
T L M I Q E R G D K \diamond V T M G Q S S A R M K L N W A V A A G 390
1171 GCCGAGGATCCAGGCCCGCGCTGGCGGCATCCTCTCCATCCAGAACATGACGACATTTGCGCCAATGCCTCTTGAACCTGCATTCC
A E D P G P A V A G I L S I Q \diamond M T T L L A \diamond A S L N L H S 420
1261 AAGAAGCAAGCCGAACCTGGAGGAGATATGAAGCAGCATCCGTGGTGTCCTCAACTCAGACGCCCTCTGCGCTCAACTCCATCTTTCTG
K K Q A E L E I Y E S S I R G V Q L R R L S A V N S I F L 450
1351 AGCCACAACAACCAAGAACTCAACTCCCCATCCTTTTCGCCCTTCTCCACCTTGAGTCCTCCGATGGGAGCGGGAAGAGACCCCT
S H N \diamond T K E L N S P I L F A F S H L E S S D G E A G R D P 480
1441 CCTGCCAAGGACGTGATGCCCTGGCCACGGCAGGAGTGCTCTGTGCCCTTCTGGAAGAGTGACAGCGACAGGGAGGCACTGGGCCACC
P A K D V M P G P R Q E L L C A F W K S D S D R G G H W A T 510
1531 GAGGGCTGCCAGGTGCTGGGCAGCAAGAACGGCAGCACCACTGCCAATGCAGCCACCTGAGCAGCTTTGGATCCTTATGGCTCATTTAT
E G C Q V L G S K \diamond G S T T C Q C S H L S S F A I L M A H Y 540
1621 GACGTGGAGGACTGGAAGCTGACCTGATCACCAAGGTGGGACTGGCGCTGTCACTCTTTCGCTGCTGTGTCATCCTCACTTTCCCTG
D V E D W K L T L I T R V G L A L S L F C L L C I L T F L 570
1711 CTGTCGGGCCCCATCCAGGGCTCGCGCACCAACCATACACCTGCACCTCTGCATCTGCCCTTTCGTTGGGCTCCACCATCTTCTGGCCCGC
L V R P I Q G S R T T I H L H L C I C L F V G S T I F L A G 600
1801 ATCGAGAACGAAGCGGCGGCTGGGCTGGCTGCCCTGGTGGCGGGCTGCTGCACCTACTGTTTCTGGCGGCCCTTCTGCTGGATG
I E N E G G Q V G L R C R L V A G L L H Y C F L A A F C W M 630

FIG. 1B

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FIG. 1A
FIG. 1B
FIG. 1C

FIG. 1

1891 AGCCTCGAAGGCCTGGAGCTCTACTTTCTTGTGGTGGCGGTGTTCCAAGCCAGGCGCTGAGTACGCGCTGGCTCTGCCCTGATCGGCTAT
S L E G L E L Y F L V V R V F Q G Q G L S T R W L C L I G Y 660

1981 GCGTGGCCCTGCTCATCGTGGCGTCTCGGCTGCCATCTACAGCAAGGCTACGGCCGCCAGATACCTGCTGGTTGGACTTTGAGCAG
G V P L L I V G V S A A I Y S K G Y G R P R Y C W L D F E Q 690

2071 GGCCTCCTCGGAGCTTCTTGGGACCTGTGACCTTCATCATTTTGTGCAATGCTGTCTATTTTCGTGACTACCGTCTGGAAGCTCACTCAG
G F L W S F L G P V T F I I L C N A V I F V T T V W K L T Q 720

2161 AAGTTTCTGAAATCAATCCAGACATGAAGAAATTAAGAGCGGCGCTGACCATCAGCGCCATCGCGCAGCTCTTCCTGTGGGC
K F S E I N P D M K K L K A R A L T I T A I A Q L F L L G 750

2251 TGCACCTGGGTCTTTGGCCTGTTCATCTTCGACGATCGGAGCTTGGTGTGACCTATGTGTTTACCATCCTCAACTGCGCTGCGAGGCGCC
C T W V F G L F I F D R S L V L T Y V F T I L N C L Q G A 780

2341 TTCCTCTACCTCCACACGCTCTGGCACTGGCCACAATCAGACCCGGCCCTCAGGGCATCAGAGTCCGGCATATGAAGGCGCATGGTT
F L Y L L L H C L L N K K V R E Y R K W A C L V A G S K Y 810

2431 TCAGAAATTCACCTCCACACGCTCTGGCACTGGCCACAATCAGACCCGGCCCTCAGGGCATCAGAGTCCGGCATATGAAGGCGCATGGTT
S E F T S T S G T G H N Q T R A L R A S E S G I

2521 CTGGACGGCCAGCAGCTCCTGTGGCCACAGCAGCTTTGTACACGAAGACCATCCATCCTCCCTTCGTCCACCACTCTACTCCCTCCACC
2611 CTCCCTCCCTGATCCCGTGTGCCACACAGGAGGAGTGGCAGCTATAGTCTGGCACCAAGTCCAGGACACCCAGTGGGTGGAGTCGGAG
2701 CCACTGGTCTCTGCTGGTCCCTCTCTGTCTCCACCTTGTGACCCAGGCTGGGGACAGGGGCTGGCCCGAGGCTGCCAATGCAGCATGTT
2791 GCCCTGGCACCTGTGGCCAGTACTCGGGACAGACTAAGGCGCTTGTCCCATCTCTGGACTTTTCTCTCATGTCTTTGCTGCAGAACTGA
2881 AGAGACTAGGGCTGGGCTCAGCTTCCCTCTTAAGCTAAGACTGATGTACAGGGCCCCATGGCGAGGCCCTTGGGGCCCACTGCCTGAG
2971 GCTCAGGTACAGAGGCCCTGCCCTGCCCTGGCCGGCAGGAGTTCTCACTGTTGTGAAGGTTGTAGACGTTGTGTAATGTGTTTTTATCT
3061 GTTAAATTTTTCAGTGTGACACTTAAATTAACACATGCATACAG

FIG. 1C



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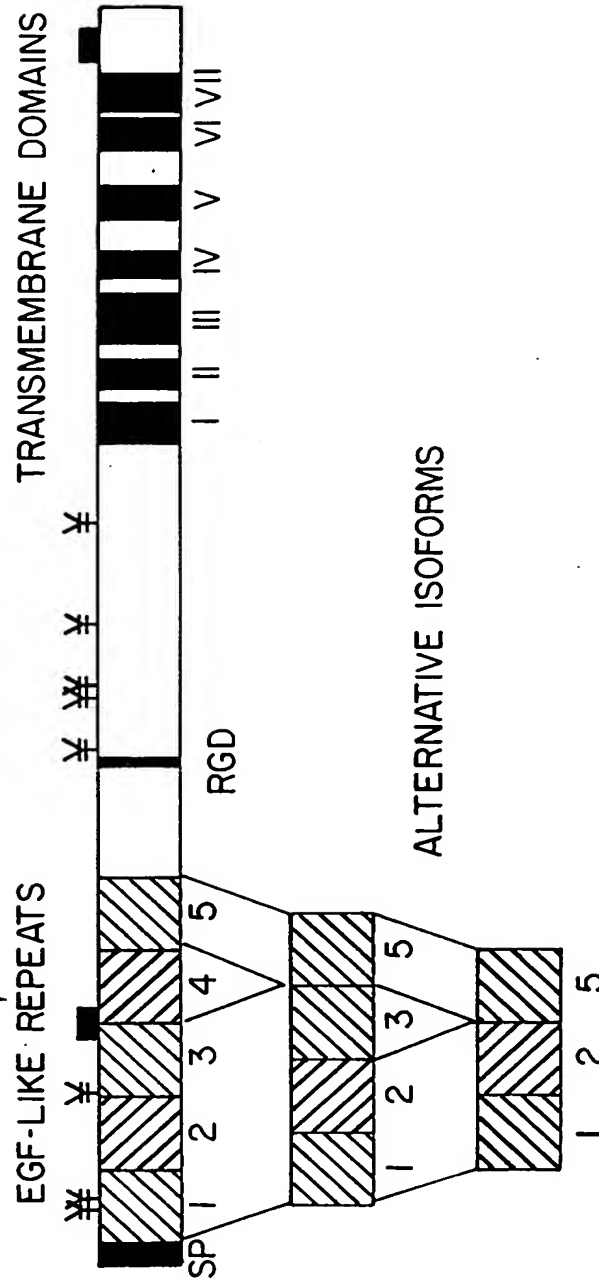


FIG. 2.



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EGF#1	DSRGCARW....CPQNSSCVNATA...CRCNPGFSFSEIITPTE...TCD
EGF#2	DINECATPSKVSCKGKFCDCWNTGSDYDCVCSPGYEPVSGTKTFKNESENTCQ
EGF#3	DVDECCQNRL.CKSYGTCVNTLGSYTCQCLPGKFIP.....EDPKVCT
EGF#4	DVNECTSGQNP.CHSSTHCLNNGSYQCRCPGWQPIPGSPNGPNT..VCE
EGF#5	DVDECSGQHQ.CDSSTVCFNTVGSYSRCRCRPGWKRPHGIPNNQKDT..VCE
Fibrillin	DIDEC-----C--G-.C-NT-GSY-C-C--GF-----C.
EMR1	DIDEC-----C-----C-N--G-Y-C-C--GF-----C
(repeat 2-6) VN *	* * * * *

D E/N β hydroxylation consensus
CXDXXXXXXCXC
(N) (E)

FIG 3

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EGF#1	DSRGCARW....CPQSSCVNATA...CRCNPGFSSFSEIITPTE...TCD
EGF#2	DINECATPSKVSCGKFSDCWNTGSDYDCVCSPGYEPVSGTKTFKNESENTCQ
EGF#3	DVDECQQNPRL.CKSYGTCVNTLGSYTCQCLPGFKFIP.....EDPKVCT
EGF#4	DVNECTSGQNP.CHSSTHCLNNVGSYQCRCPGWQIPGSPNGPNNT..VCE
EGF#5	DVDECSSGQH.Q.CDSSTVCFTVGSYSCRCRPGWKPRHGIPNNQKDT..VCE
FIBRILLIN	DIDEC-----C--G-.C-NT-GSY-C-C--GF-----C.
EMR1	DIDEC-----C-----C-N--G-Y-C-C--GF-----C
(REPEAT 2-6)	VN * * * *

D/N β
HYDROXYLATION
CONSENSUS
CXDXXXXXXCXC
(N) (E)

FIG. 3.